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**OFFICIAL COMMUNICATION
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GROUP 1646 FAX NO: 703 872-9306

Number of pages including this page 5

Applicant : Short, et al.
Serial No. : 09/997,807
Filed : November 30, 2001

Art Unit : 1646
Examiner : Michael Borin, Ph.D.

FACSIMILE COMMUNICATION

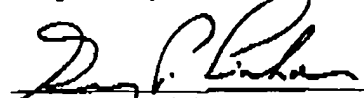
Title : Method of Making a Protein Polymer and Uses of the Polymer

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

Attached to this facsimile communication cover sheet is an Appendix A to supplement Applicants' Preliminary Amendment and Response to Restriction Requirement faxed yesterday October 29, 2003; this Appendix A being faxed this 30th day of October, 2003, to Group 1646, the United States Patent and Trademark Office.

Respectfully submitted,


Gregory P. Einhorn
Reg. No. 38,440

Date: October 30, 2003

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CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to DNA

Sequence format is Pearson

Sequence 1: SEQID_1 624 bp

Sequence 2: SEQID_3 513 bp

Sequence 3: SEQID_5 537 bp

Sequence 4: SEQID_7 395 bp

Sequence 5: SEQID_9 372 bp

Start of Pairwise alignments

Aligning...

Sequences (2:3) Aligned. Score: 78

Sequences (1:2) Aligned. Score: 80

Sequences (4:5) Aligned. Score: 70

Sequences (3:4) Aligned. Score: 67

Sequences (2:4) Aligned. Score: 66

Sequences (3:5) Aligned. Score: 78

Sequences (2:5) Aligned. Score: 79

Sequences (1:3) Aligned. Score: 76

Sequences (1:4) Aligned. Score: 62

Sequences (1:5) Aligned. Score: 63

Guide tree file created: [clustalw.dnd]

Start of Multiple Alignment

There are 4 groups

Aligning...

Group 1: Sequences: 2 Score:5182

Group 2: Sequences: 2 Score:7433

Group 3: Sequences: 3 Score:7603

Group 4: Sequences: 5 Score:4901

Alignment Score 20690

CLUSTAL-Alignment file created [clustalw.aln]

CLUSTAL W (1.81) multiple sequence alignment

```

SEQID_7  -----
SEQID_9  -----
SEQID_1  GTGAAGTACACAACCCTAGCTATAGCGGGTATTATTGCCCTCGGCTGCCGCCCTCGCCCTC
SEQID_3  GTGAAGCCTACGGCTCTAGCCCTGGCTGGTATCATTGCCCTCGGCTGCCGACCTCGCCCTG
SEQID_5  ATGAGGTACACGACCCTAGCTCTGGCCGGCATAGTGGCCTCGGCTGCCGCCCTCGCCCTG

```

```

SEQID_7  -----AGCTTCTACGCCACCGGCACAGCA
SEQID_9  -----AGCTTCTACGCCACCGGCACAGCA
SEQID_1  CTAGCAGGCTTCGCCACCACCCAGAGCCCCCTCAACAGCTTCTACGCCACCGGTACAGCA
SEQID_3  CTAGCAGGCTTCGCCACCACCCAGAGCCCCGCTCAACAGCTTCTACGCCACCGGCACAGCA
SEQID_5  CTAGCAGGCTTCGCCACGACCCAGAGCCCCGCTAAGCAGCTTCTACGCCACCGGCACAGCA

```

```

SEQID_7  CAGGCAGTAAGCGAGCCAATAGACGTGGTAAGCAGCCTCGGTACG---CTAAATACTGCC
SEQID_9  GAGGCAACAAGCGAGCCAATAGACGTTGTAAGCAACCTTAACACGGCCATAGCCCCCTGCT
SEQID_1  CAGGCAGTAAGCGAGCCAATAGACGTAGAGAGCCACCT---CGGCAGCATAGCCCCCTGCT
SEQID_3  GCCGCAACAAGCGAGCCAATAGACGTAGAGAGCCACCT---CAGCAGCATAGCCCCCTGCT
SEQID_5  CAAGCAGTAAGCGAGCCAATAGACGTAGAGAGCCACCTAGACAACACCATAGCCCCCTGCT

```

*** ***** * *** ** * *

SEQID_7 GCTGGTGCACAGGTAAGCAGACGCTAGGAGACATAACAATATATGCGCACAATGACGTG
SEQID_9 GCCGGCGCCAGGGCAGCGTGGGCATAGGCAGCATAACAATAGAGAACAGACTGACGTG
SEQID_1 GCCGGCGCACAGGGCAGTGACGACATAGGTTACGCAATAGTGTGGATAAAGGACCAGGTC
SEQID_3 GCTGGCGCACAGGGCAGCCAGGACATAGGCTACTTCAACGTGACCGCCAAGGATCAAGTG
SEQID_5 GCCGGTGCACAGGGCTACAAGGACATGGGCTACATTAAGATAACTAACCAGTCAAAGTT
** ** * * * * * * * * * * * * *

SEQID_7 AACATAACAAAGCTAAAGGTCACGCTTGCTAACGCTGCACAGCTAAGACCATACTTCAAG
SEQID_9 AACGTTGTGAAGCTGAAGATAAACCCCTCGCCAACGCTGAGCAGCTAAAGCCCTACTTTCGAC
SEQID_1 AATGATGTAAAGCTGAAGGTGACCCCTGCGTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
SEQID_3 AACGTGACAAAGATAAAGGTGACCCCTGGCTAACGCTGAGCAGCTAAAGCCCTACTTCAAG
SEQID_5 AATGTAATAAAGCTGAAGGTGACTCTCGCTAACGCCGAGCAGCTAAAGCCCTACTTTCGAC
** * * * * * * * * * * * * *

SEQID_7 TACCTGATAATAAAGCTAGTAAGCCTGGAC-----AGCAACGGCAACGAG
SEQID_9 TACCTACAGATAGTGCTAAAGAGCGTTGAC-----AGCAACGAGATCAAG
SEQID_1 TACCTACAGATACAGATAACAAGCGGCTATGAGACGAACAGCACAGCTCTAGGCAACTTC
SEQID_3 TACCTACAGATAGTGCTAAAGAGCG-----AGGTAGCT--
SEQID_5 TACCTACAGCTAGTACTCACAAGCAAC-----GCCACTGGCACC---
***** ** * * *

SEQID_7 TCCGAGGAAAAGGGCATGATAACTCTATGGAAGCCTTACGCCGTGATAATACTAGACCAT
SEQID_9 GCTG-----TGCTAAGCCTCGAGAAGCCCAGCGCAGTCATAATACTGGACAAC
SEQID_1 AGCGAGACCAAGGCTGTGATAAGCCTCGACAACCCCAGCGCCGTGATAGTACTAGACAAG
SEQID_3 GACGAGATCAAGGCCGTAAATAAGCATAGACAAGCCTAGCGCCGTGATAATACTAGACAGC
SEQID_5 GACATGGTTAAGGCTGTGCTAAGCCTCGAGAAGCCTAGCGCAGTCATAATACTAGACAAC
* * * * *

SEQID_7 GAAGA-----TTTCAACAACGACA
SEQID_9 GAGGA-----CTTCCAG-----
SEQID_1 GAGGATATAGCAGTGCTCTATCCGGACAAGACCGGTTACACAAACACTTCGATATGGGTA
SEQID_3 CAGGA-----CTTCGACAG-----
SEQID_5 GATGA-----CTACGATAG-----
* ** * * *

SEQID_7 TC-----GACAAATGACGGCAACAATGACGCCAAGATA-----AGG
SEQID_9 -----GGCGGCGACAACCAAGTGCCAGATA-----GAC
SEQID_1 CCCGGTGAACCTGACAAGATAAATTGTCTACAACGAGACAAAGCCAGTAGCTATACTGAAC
SEQID_3 -----CAACAACAGAGCAAAGATA-----AGC
SEQID_5 -----CACTAACAGATACAGCTA-----AAG
* ** * * *

SEQID_7 GTTGTAGCCTACTATGAGGCTAAGGAGGGTATGCT-----
SEQID_9 GCCACCGCCTACTACGAGGCTAAGGAGGGTATGCTA-----
SEQID_1 TTCAAGGCCTTCTACGAGGCTAAGGAGGGTATGCTATTTCGACAGCCTGCCAGTGATATTTC
SEQID_3 GCCACTGCCTACTACGAGGCTAAGGAGGGCATGCTATTTCGACAGCCTACCGCTAATATTTC
SEQID_5 GTAGAAGCCTACTATGAGGCTAAGGAGGGCATGCTATTTCGACAGCCTACCAGTAATACTG

SEQID_7 -----
SEQID_9 -----
SEQID_1 AACTTCCAGGTGCTACAAGTAGGCTAA-----
SEQID_3 AACATACAGGTGCTAAGCGTCAGCTAA-----
SEQID_5 AACTTCCAGGTACTGAGCGCGCTTGCAGTCCCTTGTGGTGA

(
(

```
(
SEQID_1:0.13368,
SEQID_3:0.05931)
:0.04152,
SEQID_5:0.08657)
:0.03782,
SEQID_7:0.18976,
SEQID_9:0.10325);
```

CLUSTAL W (1.81) Multiple Sequence Alignments

Sequence type explicitly set to Protein

Sequence format is Pearson

```
Sequence 1: SEQID_2      207 aa
Sequence 2: SEQID_4      170 aa
Sequence 3: SEQID_6      178 aa
Sequence 4: SEQID_8      131 aa
Sequence 5: SEQID_10     124 aa
```

Start of Pairwise alignments

Aligning...

```
Sequences (4:5) Aligned. Score: 63
Sequences (2:3) Aligned. Score: 70
Sequences (3:4) Aligned. Score: 54
Sequences (2:4) Aligned. Score: 58
Sequences (3:5) Aligned. Score: 68
Sequences (2:5) Aligned. Score: 70
Sequences (1:2) Aligned. Score: 72
Sequences (1:3) Aligned. Score: 65
Sequences (1:4) Aligned. Score: 54
Sequences (1:5) Aligned. Score: 60
```

Guide tree file created: [clustalw.dnd]

Start of Multiple Alignment

There are 4 groups

Aligning...

```
Group 1: Sequences: 2      Score:2421
Group 2: Sequences: 3      Score:2348
Group 3: Sequences: 4      Score:1624
Group 4: Sequences: 5      Score:946
```

Alignment Score 4564

CLUSTAL-Alignment file created [clustalw.aln]

CLUSTAL W (1.81) multiple sequence alignment

```
SEQID_1  VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLS-SITPA
SEQID_3  VKPTALALAGIIASAADLALLAGFATTQSPLNSFYATGTAAATSEPIDVESHLS-SIAPA
SEQID_5  MRYTTLALAGIVASAAALALLAGFATTQSPLSSFYATGTAQAVSEPIDVESHLDNTIAPA
SEQID_9  -----SPFYATGTAEATSEPIDVVSNLNTAIAPA
SEQID_7  -----SPFYATGTAQAVSEPIDVVSLSLGL-TLNTA
*****+*****+*+*+*+*
```

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005/005

SEQID_1 AGAAGSDDIGYATVWIKDQVNDVKLVTLRANAEQLKPYFKYLQIQITSGYETNSTALGNE
SEQID_3 AGAAGSQDIGYFNVTAQDQVNVTKIKVTLANAEQLKPYFKYLQIVLKS-----EVA
SEQID_5 AGAAGGYKDMGYIKITNQSKVNVIKLVTLANAEQLKPYFDYQLVLTSN-----ATGT
SEQID_9 AGAAGSVGIGSITIENTDQVNVVVKLKITLANAEQLKPYFDYQLVLKSV-----S
SEQID_7 AGAAGGKQTLGQITIAENDVNITKLKVTLANAAQLRPYFKYLIKLVSLD-----SNGNE
***** : * : : , ** * : * : * * * : * : * : * : *

SEQID_1 SETKAVISLDNPSAVIVLDKEDIIVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILN
SEQID_3 DEIKAVISIDKPSAVIILDSQDFDSNNRAKISAT-----
SEQID_5 DMVKAVLSLEKPSAVIILDNDYDSTNKIQLKVB-----
SEQID_9 NEIKAVLSLEKPSAVIILDNEDFQGGDNQCQIDAT-----
SEQID_7 SEEKGMITLWKPYAVIILDHEDFNNDIDNDGNNDAKIR-----
* : : : : * : * : * : *

SEQID_1 FKAFYEAKEGMLFDSLPIVFNQVQLVG-----
SEQID_3 --AYYEAKEGMLFDSLPIPNIQVLSVS-----
SEQID_5 --AYYEAKEGMLFDSLPIVILNFQVLSAACSPLW
SEQID_9 --AYYEAKEGML-----
SEQID_7 VVAYYEAKEGM-----
* : * : * : *

(
(
SEQID_1:0.16476,
SEQID_3:0.10583)
;0.02956,
SEQID_5:0.15636,
(
SEQID_7:0.23354,
SEQID_9:0.12936)
;0.04464);